

#BelBi2023 • Belgrade, Serbia

# BOOK OF ABSTRACTS



## 4th Belgrade Bioinformatics Conference

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# FOREWORD

Dear colleagues and friends,

The 4th Belgrade Bioinformatics Conference - BelBi2023, where many high-quality scientific contributions were presented, has just ended. With great thanks to all participants, we now proudly present a book of abstracts that both reflects the scientific abundance and diversity of the conference and serves as a reminder of a memorable event.

Several research institutions, faculties, and scientific societies from Serbia joined forces in organizing this international conference, which covered numerous topics in computational biology, bioinformatics, and biomedical and health informatics. The main goal of BelBi2023 was to foster contact between scientists, both early stage career and senior researchers, allowing them to share experiences and latest advances in their fields. We sincerely hope that BelBi2023 has served as a platform for researchers from around the world to meet, initiate new collaborations, and expand professional contacts, and that all of you would become a part of the growing BelBi community.

We are grateful and proud to have welcomed more than 250 researchers from 21 countries. We have had 28 scientific sessions, consisting of more than 60 lectures (including eight Keynote talks), 47 presented posters, as well as three workshops and one satellite event – COST action. We have also organized seven industry lectures, including the NGS Challenge,

two Meet the Expert Sessions, and one Business Coffee Break where ten start-up companies took part. And finally, the future BIO4 campus was presented and first panel on Serbia's resources for storage and analyses of genetic data was organized.

We would like to thank all the members of the International Advisory Board and the International Program Committee for their efforts and help in making this event a success. We are very grateful to the Ministry of Science, Technological Development and Innovation of the Republic of Serbia, SAIGE project, and UNDP-Serbia for their support. Finally, the Local Organizing Committee is very grateful to all the sponsors of the conference - BGI, Illumina & Elta'90MS, PacBio & East Diagnostics, ThermoFisher Scientific & Vivogen, Huawei, Labena, DSP Chromatography, RNIDS, Telekom Srbija, Alfa Genetics, Kefo and Superlab, hoping that they will stay with us for many years to come.

Looking forward to seeing you again at the 5<sup>th</sup> Belgrade Bioinformatics Conference.

Belgrade, July 2023

*Dr. Valentina Đorđević  
& Dr. Ivana Morić,*  
On behalf of BelBi2023  
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## From multifunctionality to polypathogenicity with intrinsic disorder

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Intrinsically disordered proteins (IDPs) lack stable tertiary and/or secondary structure under physiological conditions *in vitro*. IDPs are characterized by an astonishing multi-level spatiotemporal heterogeneity, with their mosaic structure representing a complex combination of foldons, inducible foldons, morphing inducible foldons, non-foldons, semi-foldons, and unfoldons.

IDPs are highly abundant in nature and have functional repertoire that is very broad and complements functions of ordered proteins. Often, IDPs are involved in regulation, signaling and control pathways, commonly acting as hubs in protein-protein interaction networks. Intrinsic disorder is an important constituent of the proteoform concept, representing one of the important means of functional diversification of the proteinaceous products of a gene. Functions of IDPs may arise from specific disordered forms, from inter-conversion of disordered forms, or from order ↔ disorder transitions. The choice between these conformations is determined by the peculiarities of the protein environment, and many IDPs possess an exceptional ability to differently fold in a template-dependent manner. As a result, many IDPs are capable of conducting multiple functions, with such multifunctionality being linked to their spatiotemporal heterogeneity. Therefore, a correlation between protein structure and function represents a “protein structure–function continuum”, where a given protein exists as a dynamic conformational ensemble containing multiple proteoforms characterized by diverse structural features and miscellaneous functions.

IDPs are tightly controlled in the norm by various genetic and non-genetic mechanisms. Alteration in regulation of this disordered regulators are often detrimental to a cell, and many IDPs are associated with a variety of human diseases, such as cancer, cardiovascular disease, amyloidoses, neurodegenerative diseases, diabetes and others. Furthermore, many IDPs are multipathogenic, being associated with the origination and development of a number of different diseases. Therefore, there is a though-provoking interconnection between intrinsic disorder, cell signaling, and human diseases, with polypathogenicity of the involved proteins being linked to their structural plasticity and multifunctionality.

**Keywords:** intrinsically disordered protein, multifunctionality, polypathogenicity, structure-function continuum





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